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RESPONSE TO A PARTICULARLY NASTY REVIEW IN THE JOURNAL *CLADISTICS*

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ABSTRACT

An outrageous book review in the journal Cladistics by A.V.Z. Brower of "Framework for Post-Phylogenetic Systematics" by R.H. Zander lacks understanding and collegial dignity. Examples of unpleasantries and of errors of fact and logic by the reviewer are noted here. And although I have attempted a light-hearted response, this indulgent and kindly rebuttal was rejected by the editors of Cladistics. It is offered here anyway, given that there are several new and potentially important observations that warrant publication. Topics discussed in this rebuttal are identification of paternal ancestors, uncertainty in road closings, virtual storks, correctly uncertain accuracy versus wrongly certain precision, shared and serial ancestry, classical rules of thumb, and taking the fight for reason to the barricades. Paraphyly is the best friend of molecular systematics.

The review (Brower 2014) of my recently published "Framework for Post-Phylogenetic Systematics" (Zander 2013) is exactly what I expected! Cladists are famous for their derisive disapprobation of classical evolutionary systematics. Let's extract a few representative disparagements: "retrogressive," "authoritative bleating," "browbeaten," "militantly entrenched," "reactionary intransigence," "schismatic," "calumnies," "preposterous," "sentimentally favored paraphyletic groups," "spinning of scenarios," "nihilistic," "preconceived notions," "brass," "numerological justification," and, last but not least, "Zander would like to return to a pre-cladistic world where … perhaps he is not a monkey." Wow! This justifies a civilized, collegial, measured response that untangles misunderstandings.

Because I feel that future progress in theoretical systematics shall come from students, not sunk-cost-attentive, established phylogeneticists, I ask if those considering a career in systematics would want to join a group replacing discursive logic and collegial colloquy with True Believer sloganeering and personal obloquy. My book demonstrated, in my opinion, certain fatal flaws with cladistics and phylogenetics, and these should have been addressed by the reviewer, but they were not. I wrote, for instance, on p. 123 that "cladistics alone cannot determine monophyly" and in my opinion justified that comment, but there was no reasoned reply from the reviewer. This may be because standard evolutionary theory relevant to classification is process-based and involves both shared and serial ancestry, while cladistics uses only pattern-based evidence of sister-group relationships. The two approaches, though partially compatible, usually talk past each other.

In opposition to the reviewer's reproach, I do know what cladistic analysis is, having been a fifth columnist for many years, learning hidden secrets. Cladistics is derived from phenetics and thus is also an optimally dichotomous method of optimal sorting, but it uses trait transformations on a non-ultrametric tree plus outgroup selection to root the tree. This is fine, so far. Then the result, which so appealingly looks like a natural key, is turned upside down and passed off as an evolutionary tree! No, wait, it is not called that, but instead a cladogram or phylogenetic tree. This is because many of the early cladists knew perfectly well that evolution is not essentially dichotomous (but now this important knowledge has been lost to science). The result is at best a diagram of shared descent and should be modified by what

information is available about serial descent. One would not base a supposedly evolutionary classification on just shared descent, would one? Or would one?

Cladograms are the raw results of the optimally dichotomous sorting by the cladistic analytic method. A "cladogram" is thus defined as "not an evolutionary tree." Ditto for a phylogenetic tree. The relationships between the taxa analyzed are "phylogenetic relationships" not evolutionary relationships. Classification is now much affected by the cladistic method of analysis, and taxonomic names are not changed, added, or deleted to reflect new evolutionary information but to reflect new cladistic information. My book attempts to remedy this by introducing polychotomous natural keys from which *evolutionary* trees can be constructed.

Also, contrary to the reviewer's denouncement, I really do understand the difference between cladistics and phylogenetics, but I lump them (let's call the two "phylocladistics") for the same reason that sensible people lump creationism and intelligent design — they both have wrong assumptions, faulty logic, and shore up selected facts with attractive but false simplifications. For example: Evolutionary systematics, to make a cogent analogy, would produce a diagram "Al → Bob" because after a trait-transformation clustering of OTUs (in this case examining census data), we also infer from non-sister-group-informative data (birth certificates) that Al is the father of Bob. Cladists make do with just "(Al, Bob)" and call this parenthetic diagram (in the context of a larger cladogram) a representation of monophyly even though no direct ancestor-descendent relationship is presented. Phylogeneticists are more demanding, however, and insist on the model "unknown shared ancestor → (Al, Bob)."

Evolutionary systematists can infer who their immediate patristic ancestors are, which, in the case of Bob, is "Al." Cladists apparently do not care, and phylogeneticists are confused, assuming, possibly, a stork? This analogy, though intraspecific, is demonstrative of the relationships promoted by the three schools of systematics. The reviewer asserts that "spinning of scenarios"… requires "knowledge of relationships independent of the evidence in the data matrix." Science, however, deals with inferences from relevant data, and inferences from restricted data must be expected to give less than relevant results. Clearly, diagrams or models in evolutionary systematics incorporate much more evolutionarily relevant information than do those of cladistics or phylogenetics. We evolutionary systematists consider serial transformations in monophyletic groups the basic process-based feature of evolutionary analysis.

The preoccupation of cladists is to find the shortest tree. If there are two or more descendant taxa from one extant ancestral taxon, then, reasonably, a longer tree is required. Cladists' zeal is misdirected, and maximum parsimony actually masks multiple serial transformations such as bursts of adaptive radiation from a single ancestral taxon. Phylogeneticists have somewhat the same preoccupation but additionally contend over whether it was the same or different storks that brought Al and Bob. There are no storkish ad hoc inventions in caulograms or Besseyan cacti of serial macroevolutionary transformations, although the postulation of unknown ancestral taxa is acceptable when justified by inference (not as a structural part of the phylogenetic method).

The reviewer avers that support for clades should be empirical, not warm and fuzzy group favoritism. So, another analogy: Consider a salesman who wants to visit several cities by the shortest route and needs to know how much money to take for gasoline. The optimal route is the solution to the classical traveling salesman problem, and support for the shortest route may be based solely on distances (how much better the shortest route is than the next shortest, and so on). Thus, support is measured by information already in the data set. But suppose information not relevant to the distance between cities is also available, for instance, roads connecting various cities are sometimes closed when you show up in your car but you know what the probability of closure is for each road and you thus know which roads to avoid. Optimality judged only from the data set on road lengths can be more *precise* than total evidence involving uncertainty with other information, but *accuracy* based on total evidence can be critical in

decisions even when there is more uncertainty when all data are examined. Cladograms are precise but you can run out of gas.

The reviewer complains about my "downweighting of the empirical evidence." Scientific theories must address all evidence, including that which is not in the cladistic data set. Yes, they must. Eliminating evidence for serial ancestry does not make sister-group evidence the only empirical evidence available. Scientific inference using induction and analogy does not result in "preconceived notions" but along with deduction can help develop a process-based theory of evolutionary transformation that results in a better, testable classification that predicts where new taxa will fit into the theory.

The reviewer asserts that I offer "a method for differentiating (morpho)species in terms of the geometric mean and Fibonacci series." No such thing. I suggested instead that classical taxonomists have used such as a part of a heuristic method for writing descriptions for many years, not realizing the fundamental physical and mathematical reason for their doing so. Powerful and useful heuristics underlie the methods of classical systematics.

It has been said that, in long-running listserver arguments between systematists, eventually someone calls someone else a Nazi. I would never do this. Instead, I have devised a 10-degree Scale of Evil. The Scale is exponential, as in the Richter Scale (base 10). As with earthquakes, a three is the minimum detectable event of evil, rarely very damaging, such as turning your head from an instance of social injustice, not giving a beggar a buck when you probably should have, or hurting someone's feelings and not fixing it. Four to 4.9 is light damage, 5 to 5.9 is moderate with few casualties, 6 to 6.9 is strong with up to 25,000 dead, 7 to 7.9 is major with up to 250,000 dead, 8 to 8.9 is great with large cities decimated, and 9 or more is total destruction. A ten would be a paper I found by A. Hitler (no citation to protect innocent minds) vigorously defending brutality in service of the state.

Are major cladistic classification changes that are due to avoidance of paraphyly and implementation of strict phylogenetic monophyly truly harmless? Or perhaps shall they have a high rating on the Scale of Evil for elimination of inferable ancestor-descendant relationships? Should we classify the polar bear as a brown bear, or not? Is a cactus just another portulaca? Celebrity species can be dealt with case by case, but there are myriad small, less well-known families, genera, and species that have fallen to epistemological extinction due to misplacement, or synonymization, or crowded into anonymity among a number of new, trivial molecular or cryptic families, genera, and species. The specialist reader can doubtless name some, and he should assess damage and raise a squawk.

In my own case, the moss family Pottiaceae of 76 genera that I've studied for 50 years has had three related families involving three genera dumped into it by molecular systematists, another two genera excised to a new family, one genus buried in another, and another genus split into four, all due to a desire to eliminate paraphyly in molecular cladograms. Although occasionally minor morphological traits are trotted out that appear to support such classification changes, no support is possible from morphological traits that cannot together stand on their own in distinguishing taxa, particularly when another explanation of the molecular paraphyly is possible, namely serial descent. Conversely, no molecular classification can falsify a morphological one unless it itself can stand alone (without morphological input), which presently is laughable, given poor sampling and no islands of stability in a sea of cladogram branches. Given that a cladistic earthquake affected nine of the 76 genera of Pottiaceae, this is clearly more than a few casualties, and I can easily assign a 6.5 on the Scale of Evil for that large family, and a 10 for each of the three blasted smaller families. Readers may wish to rate their own groups of specialization as to the effect of strict phylogenetic monophyly in destroying, inventing, or displacement of taxa, perhaps on a similar Scale, or alternatively, use a Holophyletic Scale of Truth and Light if they have the brass.

The reviewer "found it tiresome to be browbeaten with redundant claims about the supposed shortcomings of molecular systematics … ." Ridiculous. I pointed out clearly that molecular systematics has introduced two quite powerful analytic tools: (a) distance on a cladogram greater than expected extinct paraphyly, and (b) known paraphyly interpretable as an ancestor-descendant relationship. Paraphyly is the best and perhaps only friend of molecular analysis. Everything else, of course, either reflects preselection of OTUs with known classical relationships or may be considered aleatory.

"Zander frequently repeats his arguments, sometimes almost verbatim and at length." Exactly. This is justified in the Introduction in that the catharsis needed for deprogramming is facilitated by repetition, shame, and appeals to reason. "Zander is one of a small group [of] militantly entrenched advocates of paraphyly … ." The advocates of evolutionary systematics, I might remind the reviewer, are a small group only if they are narrowly defined as paraphyly-huggers. Most practicing taxonomists do alpha taxonomy without any particular investment in cladistics or phylogenetics, but I do get occasional thanks from them for taking the fight for reason to the barricades. I have noted, in addition, a general unease or even cynicism among classical botanists when I inquire if they were ever asked to vote as to whether their institution's herbaria are to be re-ordered according to the latest APG phylogenetic classification or be arranged by some more sensible system like an updated version of that of Thorne or Takhtajan.

The reviewer asserted that "a book review is not the forum for a full-fledged refutation of a schismatic research programme." Why not? I made only a few major suggestions of how to fix systematics by combining the best of classical, cladistic, and phylogenetic methods. Such is only schismatic if all systematists were cladists now, which is an arrogant conceit on the part of cladists that one reads often in the literature. The reviewer carefully avoided substantive criticism of my emphasis on process-based causal theory, heterophyletic inference of deep ancestors, self-nesting ladders, superoptimization, treating heuristics as powerful analytic tools based on physics, treating the genus as a basic unit of evolution, and the danger to conservation and biodiversity research of classifications based only on sister-group analysis. Surely the reader would like some rational evaluation of these from the reviewer.

I have had as much satisfaction in writing this response as the reviewer doubtless had in crafting his acerbic review. The issues, however, are serious. Changes made in classifications have been considered of little consequence because classifications are easily modified if wrong. But in the context of the need for scientific guidance during a world extinction event, wrong though potentially corrigible classifications, even if ephemeral, can greatly affect conservation planning, triage, political decisions, and scientific evaluations of biodiversity.

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